

**FIGURE 1: EDG4 AMINO ACID SEQUENCE**

1 10 20 30 40 50  
MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTN  
51 60 70 80 90 100  
LLVIAAIASNRRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLS  
101 110 120 130 140 150  
LEGWFLRQGLLDTSLTASVATLLAVERHRSVMAVQLHSRLPRGRVVML  
151 160 170 180 190 200  
IVGVWVAALGLGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLV  
201 210 220 230 240 250  
FLLMVAVYTRIFFYVRRRVQRMAEHVSCHPRYRETTLSLVKTVVILGAF  
251 260 270 280 290 300  
VVCWTPGOVVLLDGLGCESCNVLAVEKYFLLIAEANSLVNAAVYSCRDA  
301 310 320 330 340 350  
EMRRTFRRLLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMTPP  
351 360 370 380  
FSYLELQRYAASNKSTAPDDLWVLLAQPNQD

**FIGURE 2: EDG4 NUCLEOTIDE SEQUENCE**

1 ggcacgaggc gccgggcat gggcctcgag cccgccccga acccccgcga gccgccttg  
61 tctgcggcgt gactggaggc ccagatggtc atcatggcc agtgcacta caacgagacc  
121 atcggcttct ttataaaca cagtggcaa gagctcagct cccactggcg gccaaggat  
181 gtggtcgtgg tggactggg gctgaccgtc agcgtgctgg tgctgctgac caatctgctg  
241 gtcatacgag ccatacgcc tc aaccgcgc ttccaccgc ccactctacta cctgctcgcc  
301 aatctggccg cggctgaccc ttccgggc gtggctacc tcttcctcat gttccacact  
361 ggtccccgca cagccccact ttcaacttgc ggtggttc tgccgcaggg cttgctggac  
421 acaaggctca ctgcgtcggt ggcacactg ctggccatcg ccgtggagcg gcaccgcagt  
481 gtatggccg tgca gctgca cagccgcctg ccccggtggc gcgtggcat gctattgtg  
541 ggcgtgtgg tggctgcct gggctgggg ctgctgcctg cccactcctg gcactgcctc  
601 tgtgcctgg accgctgctc acgcattggca ccctgctca gccgtcccta tttggccgtc  
661 tgggtctgt cgacgcgtc tgtcttcctg ctcatggtg ctgtgtacac ccgcattttc  
721 ttctacgtgc ggcggcgagt gcagcgcattt gca gacatgc gca gacatgc tca gctgtgc  
781 cgagagacca cgctcagct ggtcaagact gttgtcatca tcctgggggg gttctgggt  
841 tgcgtggacac caggccaggt ggtactgctc ctggatgggt tagctgtga gtcctgcaat  
901 gtcctgggtg tagaaaaatg cttctactg ttggccgagg ccaactact ggtcaatgt  
961 gctgtgtact cttggccgaga tgctgagatg cgccgcaccc tccgcgcct tctctgtgc  
1021 gctgcctcc gca gtcgtccac cccgcgactt gtcactata catccctctgc ccaggaggt  
1081 gca gacactc gcatcatgt tcccgagaa ggcacccac tgatgactcc accctttagc  
1141 taccttgaac ttca ggggttca cggcgcagg aacaatcca cagccctgtg tgacttgtgg  
1201 gtcgtcctgg ctc aacccaa ccaacaggac tgactgactg gcaggacaag gtcggcatg  
1261 gca cagcacc actgcccaggc ctccccaggc acaccactt gcccaggaa tgggggcttt  
1321 ggg tcatctc ccaactgcctg ggggagtcag atgggtgc ggaatctggc tcttcagcca  
1381 ttc tca ggtt aggggggttta aacagacat tattctgttt tcactgcgtt tccttggtaa  
1441 gccctgtgg a cttgggttctg ctgtgtatg ctgagggttt taagggtgggg agagataagg  
1501 gctctctcgg gca tgcgttac cccgttatgac tgggtatga ggacagactg tggacacccc  
1561 atctacactg a gtcgtattt ttagcagcag agactgagggt gtcagatgt tgagctggg  
1621 aagg tttgtg gtccttgc gctccagg actggcctgt ccccaataga atgaagcag  
1681 tccacgggaa gggatgata caaggatgaa acctttctt acactcaaaa aaaa

### **FIGURE 3: EDG5 AMINO ACID SEQUENCE**

1 MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILCCAIVVE  
 10  
 20  
 30  
 40  
 50  
 51 NLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRL  
 60  
 70  
 80  
 90  
 100  
 101 TPVQWFAREGSASITLSASVFSLLAIAIAIERHVIAIKVKLYGSDKSCRMLL  
 110  
 120  
 130  
 140  
 150  
 151 LIGASWLISLVLGGLPILGWNLGHLEACSTVLPYAKHYVLCVVTIFS  
 160  
 170  
 180  
 190  
 200  
 201 ILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLGVFIVCWLPAF  
 210  
 220  
 230  
 240  
 250  
 251 SILLLDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL  
 260  
 270  
 280  
 290  
 300  
 301 RPLQCWRPGVGQGRRRVGTPGHLLPLRSSSSLERGMHMPTSPTFLEGN  
 310  
 320  
 330  
 340  
 350  
 351  
 361

**FIGURE 4: EDG5 NUCLEOTIDE SEQUENCE**

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1 atggggcagct tgtactcgga gtacacctgaac cccaaacaagg tccaggaaca ctataattat
61 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcata
121 gtcatcctct gttgcgccat tgtgggtggaa aaccttctgg tgctcatatgc ggtggcccgaa
181 aacagcaagt tccactcgac aatgtacactg tttctgggca acctggccgc ctccgatcta
241 ctggcaggcg tggccttcgt agccaaatacc ttgtcttcgt gctctgtcac gtcgagggtcg
301 acgcctgtgc agtgggttgc cggggagggc tggccttcca ttcacgctctc ggcctctgtc
361 ttcaagctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat
421 ggcagcgcaca agagctgcgc catgcttctg ctcatacgggg ctcctgtggct catctcgctg
481 gtcctcggtg gcctgccccat ctttggtctgg aactgcctgg gccacacctcgaa
541 actgtcctgc ctctctacgc caagcattat gtgctgtcg gtgtgaccat ctctccatc
601 atcctgttgg ccatcggtgc cctgtacgtg cgcatactact gcgtggtccg ctcaagccac
661 gctgacatgg cggcccccgc gacgctagcc ctgctcaaga cggtcaccat cgtgctaggc
721 gtcttatacg tctgtggct gccccgcctc agcatccccc ttctggacta tgccctgtccc
781 gtcacactct gccccgatct ctacaaagcc cactacttt tcggcgtctc caccctgaat
841 tccctgctca accccgtcat acatcactgg cgcagccggg acctgcggcg ggagggtgtt
901 cggccgctgc agtgcgtggcg gccgggggtg ggggtgcaag gacggaggcg ggtcgggacc
961 ccggggccacc acctccgtcc actccgcagc tccagctccc tggagaggggg catgcacatcg
1021 cccacgtcac ccacgtttct ggagggcaac acggtggtct qa

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**FIGURE 5: EST No. AA419064**

GGGCCATGGCTCGAGCCGCCCGACCCCCCGAGCCCGCTTGTCTCGGGCGTGACTGG  
AGGCCAGATGGTCATCATGGGCCAGTGTACTACAAACGAGACCATCGGCTTCTTCTATA  
ACAACAGTGGCAAAGAGCTCAGCTCCCACTGGCGGCCAACGGATGTGGTCGTGGCAC  
TGGGGCTGAGCGTCAGCGTGTGGTCGTGACCAATCTGCTGGTCATAGCAGGCATCG  
CCTCCAAACGCCGCTTCCACAGCCCCATCTACTACCTGCTCGGAATCTGGCCGGCTG  
ACCTCTCGGGCGTGGCTACCTCTCCATGTTCCACACTGGTCCCCGACAGCCCC  
ACTTCACTTGAGGG